



1600

#6

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/785,474A

DATE: 11/18/2002 TIME: 12:52:34

Input Set : A:\Sub\_Seq\_List\_0609\_4180002.txt
Output Set: N:\CRF4\11182002\1785474A.raw

|     | 5   | <:110> | > AP                           | PLIC  | CANT  | : Tai | nzi,    | Rudo  | olph  |       |       |       |     |            |     |       |            |          |
|-----|-----|--------|--------------------------------|---|-------|-------|---------|-------|-------|-------|-------|-------|-----|------------|-----|-------|------------|----------|
|     | 6   |        | Wa                             | Wasco, Wilma  |       |       |         |       |       |       |       |       |     |            |     |       |            |          |
|     | 9   | <:120> | > TI                           | TITLE OF INVENTION: Genetic Alterations Related To Familial Alzheimer's Disease |       |       |         |       |       |       |       |       |     |            |     |       |            |          |
|     | 11  | <:130> | > FI                           | FILE REFERENCE: 0609.4180002  |       |       |         |       |       |       |       |       |     |            |     |       |            |          |
|     | 14  | <:140> | > CU                           | RREN  | IA TI | PLIC  | CATIO   | ON NO | JMBEI | R: 09 | 9/78  | 5,474 | 4 A |            |     |       |            |          |
|     | 15  | <141>  | > CU                           | RREN  | IT F  | LING  | G DAT   | ΓE: 3 | 2001  | -02-2 | 20    |       |     |            |     |       |            | RECEIVE  |
|     | 18  | <:150> | > PR                           | IOR   | APPI  | LICA  | TION    | NUM   | BER:  | US (  | 08/70 | 06,34 | 1.4 |            |     | ì     | Г          |          |
|     | 19  | <:151> | > PR                           | IOR   | FIL   | ING I | DATE    | 199   | 96-0  | 3-30  |       |       |     |            | 5   | V     |            | 41/51    |
|     | 22  | <:150> | > PR                           | IOR   | APPI  | ICA   | TION    | NUM   | BER:  | US (  | 60/00 | 03,09 | 54  |            | Ĵ   |       |            | NOV > 4  |
|     | 23  | <151>  | > PR                           | PRIOR FILING DATE: 1995-08-31   |       |       |         |       |       |       |       |       |     |            |     |       |            | A        |
|     | 26  | <160>  | > NUI                          |   |       |       |         |       |       |       |       |       |     |            |     |       | <u>[E0</u> | A CENTER |
|     | 29  | <170>  | SOFTWARE: PatentIn version 3.1 |   |       |       |         |       |       |       |       |       |     |            |     |       |            |          |
|     | 3.2 | < 210> | > SEQ ID NO: 1                 |   |       |       |         |       |       |       |       |       |     |            |     |       |            |          |
|     | 3.3 | <:211> | 1> LENGTH: 2765                |   |       |       |         |       |       |       |       |       |     |            |     |       |            |          |
|     | 34  | <:212> |                                |   |       |       |         |       |       |       |       |       |     |            |     |       |            |          |
|     | 35  | <213>  | > ORG                          | GANI  | SM:   | Homo  | sap     | oiens | 5     |       |       |       |     |            |     |       | $\vdash N$ | ERED     |
|     | 38  | <220>  | 0> FEATURE:                    |   |       |       |         |       |       |       |       |       |     |            |     |       |            |          |
|     | 39  | <221>  | NAME/KEY: CDS                  |   |       |       |         |       |       |       |       |       |     |            |     |       |            |          |
|     | 4() | <:222> | > LOCATION: (249)(1649)        |   |       |       |         |       |       |       |       |       |     |            |     |       |            |          |
|     | 41  | <:223> | OTHER INFORMATION:             |   |       |       |         |       |       |       |       |       |     |            |     |       |            |          |
| - > | 44  | <400>  | 1                              |   |       |       |         |       |       |       |       |       |     |            |     |       |            |          |
|     |     |        |                                | -   | -     |       | -       |       |       |       |       |       |     |            |     |       | ggtctg     | 60       |
|     |     |        |                                |   |       | _     | -       |       |       | _     |       |       |     |            |     |       | cctaat     | 120      |
|     |     |        | -                              | _   | -     |       |         |       |       |       |       | _     | _   |            |     |       | aggaga     | 180      |
|     |     |        |                                |   | -     |       |         |       |       | _     |       | _     |     |            |     |       | atacag     | 240      |
|     |     | ttgct  | cca                            |   |       |       |         |       |       |       |       |       |     |            |     |       |            | 290      |
|     | 54  | 1      |                                |   |       |       |         |       |       |       |       |       |     |            |     |       |            |          |
|     | 5.5 |        |                                | 1   |       |       |         | 5     |       |       |       |       | 10  |            |     |       |            |          |
|     |     | cag a  | _                              |   |       | _     |         |       | _     | _     |       |       | -   |            | -   | _     |            | 338      |
|     |     | Gln M  | let s                          | Ser   | Glu   | Asp   |         | His   | Leu   | Ser   | Asn   |       | Val | Arg        | Ser | Gln   |            |          |
|     | 59  |        |                                |   |       |       | 20      |       |       |       |       | 25    |     |            |     |       | 30         |          |
|     |     | gac a  |                                | _   | _     |       | -       |       |       |       |       | -     |     |            |     |       |            | 386      |
|     |     | Asp A  | sn A                           | Arg   | Glu   | _     | GIn     | Glu   | His   | Asn   | -     | Arg   | Arg | Ser        | Leu | _     | His        |          |
|     | 6.3 |        |                                |   |       | 35    |         |       |       |       | 40    |       |     |            |     | 45    |            |          |
|     |     | act g  |                                |   |       |       |         |       |       |       | _     |       |     |            |     |       |            | 4 3 4    |
|     |     | Pro G  | Slu I                          | Pro   |       | Ser   | Asn     | Gly   | Arg   |       | Gln   | GIY   | Asn | Ser        |     | GIn   | Val        |          |
|     | 67  |        |                                |   | 50    |       |         |       |       | 55    |       |       |     |            | 61) |       |            | 4.0.2    |
|     |     | gtg g  |                                |   |       |       |         |       |       |       |       |       |     |            |     |       |            | 482      |
|     |     | Val G  |                                |   | Asp   | GIu   | 11 [ ز) | GTu   | _     | G1u   | GTU   | Leu   | ınr |            | LYS | ıyr   | GIY        |          |
|     | 71  |        |                                | 55  |       |       |         |       | 70    | _+-   |       | ~+~   | 20+ | 75<br>5t 6 | +   | a t = | a+ a       | E 3.0    |
|     |     | gcc a  |                                |   |       |       |         |       |       |       |       |       |     |            |     |       |            | 530      |
|     | 74  | Ala L  | ys E                           | 115   | val   | rre   |         | Leu   |       | val   | Pro   |       | inr | Leu        | Cys | wer   | val        |          |

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## RAW SEQUENCE LISTING

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121 ctg gtt gaa aca gct cag gag aga aat gaa acg ctt ttt cca gct etc

122 Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu

125 att tac tcc tca aca atg qtg ttg gtg aat atg gca gaa gga gac 126 Ile Tyr Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp

129 ccg gaa gct caa agg aga gta tcc aaa aat tcc aag cat aat gca gaa

130 Pro Glu Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu
131 305 310 315
133 agc aca gaa agg gag tca caa gac act gtt gca gag aat gat gat ggc

134 Ser Thr Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly

137 ggg ttc agt gag gaa tgg gaa gcc cag agg gac agt cat cta ggg cct

138 Gly Phe Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro

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DATE: 11/18/2002 474A TIME: 12:52:34

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Output Set: N:\CRF4\11182002\I785474A.raw

77 qtq qtc qtq qct acc att aaq tca qtc agc ttt tat acc cgg aag gat

| 78 Val Val Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp 79 95 100 105 110   |      |
|--|------|
| 81 ggg cag cta atc tat acc cca ttc aca gaa gat acc gag act gtg ggc<br>82 Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly                       | 626  |
| 83 115 120 125<br>85 cag aga geo etg cac tea att etg aat get geo atc atg atc agt gto   | 674  |
| 86 Gln Arg Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val<br>87 130 135 140   |      |
| 89 att gtt gtc atg act atc ctc ctg gtg gtt ctg tat aaa tac agg tgc<br>90 Ile Val Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys                       | 722  |
| 91 145 150 155<br>93 tat aag gtc atc cat gcc tgg ctt att ata tca tct cta ttg ttg ctg   | 770  |
| 94 Tyr Lys Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu 95 160 165 170  | 770  |
| 97 ttc ttt ttt tca ttc att tac ttg ggg gaa gtg ttt aaa acc tat aac<br>98 Phe Phe Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn<br>99 175 180 185 190 | 818  |
| 101 gtt gct gtg gac tac att act gtt gca ctc ctg atc tgg aat ttt ggt 102 Val Ala Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly 103 200 205            | 866  |
| 105 gtg gtg gga atg att tcc att cac tgg aaa ggt cca ctt cga ctc cag 106 Val Val Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln 107 210 215 220        | 914  |
| 109 cag gca tat ctc att atg att agt gcc ctc atg gcc ctg gtg ttt atc<br>110 Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile<br>111 225 230 235  | 962  |
| 113 aag tac ctc cct gaa tgg act gcg tgg ctc atc ttg gct gtg att tca 114 Lys Tyr Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser 115 240 245 250        | 1010 |
| 117 gta tat gat tta gtg gct gtt ttg tgt ccg aaa ggt cca ctt cgt atg<br>118 Val Tyr Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met                     | 1058 |

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Input Set : A:\Sub\_Seq\_List\_0609\_4180002.txt
Output Set: N:\CRF4\11182002\1785474A.raw

| 143  |     | His Ar  | g Ser  | Thr   |            | Glu   | Ser   | Arg   | Ala   | Ala<br>360 | Val   | Gln    | Glu    | Leu   | Ser<br>365 | Ser   |              |
|--|-----|---------|--------|-------|------------|-------|-------|-------|-------|------------|-------|--------|--------|-------|------------|-------|--------------|
| 146   Ser   Tie   Leu Ala Gly Glu Asp   Pro Glu Glu Arg Gly Val   Lys   Leu Gly   147   370   375   380   385   380   395      |     | 201 21  | a ata  | aat   |            |       | aza   | 002   | ana   |            | 3/1/0 | aaa    | ata    | 222   |            | aa a  | 1304         |
| 147   370   375   380   375   380   375   149    |     | -       |        | -     |            | -     | -     |       |       |            |       |        |        |       |            |       | 1374         |
| 149 ttg gga gat ttc att ttc tac agt gtt ctg gtt ggt aaa gcc tca gca   1442   |     | 3e1 11  | e Leu  |       | GIY        | GIU   | АЗР   | FIO   |       | GIU        | лгу   | ,3 T Å | vai    |       | Leu        | Gry   |              |
| 150   Leu Gly Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala   151   385   390   395    |     | tta aa  | a dat  |       | att        | ttc   | tac   | agt   |       | cta        | att   | aat    | ааа    |       | tca        | aca   | 1442         |
| 151  |     |         |        |       |            |       |       |       |       |            |       |        |        |       |            |       | 1112         |
| 153 aca gcc agt gga gac tgg aac aca acc ata gcc tgt ttc gta gcc ata 154 Thr Ala Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile 155 400 405 410 405 157 tta att ggt ttg tgc ctt aca tta tta ctc ctt gcc att ttc aag aaa 158 Leu Ile Gly Leu Cys Leu Thr Leu Leu Leu Leu Leu Ala Ile Phe Lys Lys 159 415 420 425 430 161 gca ttg cca gct ctt cca atc tcc atc acc ttt ggg ctt gtt ttc tac 162 Ala Leu Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr 163 435 440 445 165 ttt gcc aca gat tat ctt gta cag cct ttt atg gac caa tta gca ttc 166 Phe Ala Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe 167 450 455 460 169 cat caa ttt tat atc tagcatatt gcggttagaa tcccatggat gtttctctt 173 tqactataac caaatctgg gaggacaaag gtgattttc tgtgtccaca tctaacaaag 1749 175 tcaagttcc cggctggact tttgcagat ccttccaagt cttcctgacc accttgcact 175 tcaagttcc cggctggact tttgcagat gcctatagaa aacgatttg aacatactc atcgcagtgg 179 actgtgtccc tcqgtgcaaa aactaccaga tttgaggag gaggtcaagg agatadgat 183 gacactgga actctcagga ctaccaggt ccatcagacag caggtcaagg agatadgat 1849 187 aagttctdaa cttttcaaga acctgttaga gaaggacaaggt ggtatttcc tgtgtccaca tctaacaaag 188 gacactgga actcttcaag ccaacaaga tttgaggac gaggtcaagg ggtattacat 189 agattctgaa cttttcagag gytactgtga ggaagadgag ggtattacat 189 agattctgaa cttttctaga ggtagaaggt ggaagaaggag ggaatatgat 189 accgagaag tgggagggg ttccaaggt ggaagaagagg ggtagaagggggggggg   |     | Dea or  | _      |       | 110        | 1     | * I * |       | , 41  | De u       | ,     | 311    |        |       | 001        |       |              |
| 154 Thr Ala Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile  |     | aca ge  |        | gga   | gac        | taa   | aac   |       | acc   | ata        | qcc   | tat    | ttc    | qta   | qcc        | ata   | 1490         |
| 155  |     |         |        |       |            |       |       |       |       |            |       |        |        |       |            |       |              |
| 157  |     |         |        | 4     |            | -     |       |       |       |            |       |        |        |       |            |       |              |
| 158   Leu   Ile   Gly   Leu   Cys   Leu   Thr   Leu   Leu   Leu   Leu   Ala   Ile   Phe   Lys   Lys   A30   A25   A30   A30   A25   A30   A30   A30   A30   A30   A30   A30   A30   A30   A35   A40   A45   A40   A45   A45   A46   A45   A46   A45   A46   A46   A45   A46   A45   A46   A45   A46   A46   A45   A46   A45   A46   A45   A46    |     | tta at  | t ggt  | ttg   | tqc        | ctt   | aca   | tta   | tta   | ctc        | ctt   | gcc    | att    | ttc   | aag        | aaa   | 1538         |
| 1586 161 gca ttg cca gct ctt cca atc tcc atc acc ttt ggg ctt gtt ttc tac 162 Ala Leu Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Pro Tr 163 435 440 445 165 ttt gcc aca gat tat ctt gta cag cct ttt atg gac caa tta gca ttc 166 Phe Ala Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe 167 450 460 169 cat caa tt tat atc tagcatattt gcggttagaa tcccatggat gtttcttct 1689 170 His Gln Phe Tyr Ile 171 465 173 tqactataac caaatctggg gaggacaaag gtgattttcc tgtgtccaca tctaacaaag 1749 175 tcaagattcc cgggtggact tttgcagct ccttccaagt cttcctgacc accttgcact 1809 177 attggacttt ggaaggaggg gcctatagaa aacgattttg aacatacttc atcgcagtgg 1869 178 acgccggaag ttgctgtgcc ccatcagcag cttgagggg gggtcaagg agatatgata 1929 189 agacctgga actctcagga ctaccaggat ccaagaggt aggtgaagg ggttaaacca 2049 187 gaattctgaa ctttcatgaa actaccagt gaaaatcaac ccaataattc tgtattaact 2109 188 gaattctgaa ctttcagga ggtacatgg ggaggacaga cagaatgggg 189 aatqqagagg tgggcagggq ttccagctt cctttgattt tttgetgcag actcatcctt 2229 181 ggcccggaag ttgctgttc ccttcttt qagtcaagt aattagtag attgctttatc 2219 189 aatqqagagg tgggcagggq ttccagcttc cctttgattt tttgetgcag actcatcctt 2229 189 aatqqagagg tgggcagggq ttccagcttc cctttgattt tttgetgcag actcatcctt 2229 191 tttaaatgag acttgtttc cctctcttt qagtcaagtc aaattagtag attgctttg 2289 193 gcacgtctg aacctaggt tctttatcc taaaagttt aacctcagt tgattgccaa 2349 195 ggccagtctg aacctaggt tctttatcc taaaagttt aacctcagt tgattgcaaat 2349 195 ggccagtctg aacctaggt tgattttct catcaattct ctatcattgt gaagtcaaat 2469 197 gtaaattttg gaaacagtac agtatttct catcaattct ctatcattgt gaagtcaaat 2589 201 tgcctcct tgctcattc ttctctccac cacaagaggt cttttctac agccagtaag 2589 203 gcagctctgt crtygtagca gatggtcca ttattctagg gtcttacct ttgtatgatg 2649 205 aaaagaatgt gttatgaatc ggtgctgtca gccctgctgt cagaccttct tccacagca 2709 270 atgaattt gcccaaagc ggtagaatta aagaagagta aaatggctgt tgaagc 2700 270 atgaattt gcccaaagc ggtagaatta aagaagagta aaatggctgt tgaagc 2709 270 210 < 210 > SEQ ID NO: 2 271 < 212 < 212 > TYPE: PRT 271 < 213 > ORGANISM: Homo sapiens 216 < 400 > SEQUENCE: 2 271 Met Thr G |     |         |        |       |            |       |       |       |       |            |       |        |        |       |            |       |              |
| 162 Ala Leu Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr 163 435 440 445 165 ttt gcc aca gat tat ctt gta cag cct ttt atg gac caa tta gca ttc 166 Phe Ala Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe 167 450 455 460 169 cat caa ttt tat atc tagcatattt geggttagaa teccatggat gtttettet 1689 170 His Gln Phe Tyr Ile 171 465 173 tqactataac caaatctggg gaggacaaag gtgatttee tgtgtecaca tetaacaaag 1749 175 tecaagattee eggetggact tttgcagett cettecaagt etteetgace acettgeact 1809 177 attggacttt ggaaggaggt gectatagaa aacgattttg aacatactte ategcagtgg 1869 179 actgtgtee teggtgeaga aactaceaga tttgagggae gaggteaagg agatatgata 1929 181 ggeeeggaag ttgettgtgee ceateageag ettgaegggt ggtcacagga eggatteact 2049 185 aaceggaact etteatettaa actacacgtt gaaaatcaac ceaataatte tgtattaact 2109 187 gaattetgaa etttteagga ggtaetgtga ggaaggaag gaccagaag eagaatgggg 2169 189 aatqagaagag tgggeaggg ttecagette eetttgatt tttgetgeag actacteett 2239 189 gecagtetg aacettgagga ettgattee eettttgatt tttgetgeag actacteett 2239 191 tttlaaatgag acttgtttee eetteettt gagteaagte aaattatgag attgetettg 2289 193 geaattette ttetcaagaa etgacactea ttacegtetg tgattgecat ttetteecaa 2349 195 ggeeagtetg aacettgaggt tegtttatee taaaagttt aacetcaggt tegaagteettg 2289 197 gtaaattttg gaaacagtac agetattee teacaatteet tetteecaa 2409 197 gtaaattttg gaaacagtac agetatteet cateaattet tacetaetgt gaagteaate 199 ttggatttte eaceaaatte tgaatttgta gacatactte teateatgt gaagteaat 199 tgaatettte caccaaatte tgaatttgta gacatactte teateatgt gaagteaat 190 gecegtetg ertggtaga gggtetga geetteet teateatgt gaagteaat 190 gaaacagtag gggagaagga agetgtee eagaacteet teacaagea 2589 201 tgeeteete gteeteate tteeteeca cacaageag ettttetea agecagtaag 203 gaagetetgt ertggtaga gatggteea ttattetaag teacacae 269 204 tagaattga tgeecaaage ggtgetgta geetgtgt gagaecttet teacaagea 205 aaaagaatgt gttagaate ggtgetgta geetgtgt gagaecttet teacaagea 206 aaaagaatgt gttagaate ggtgetgta geetgtgt gagaecttet teacaagea 207 atgaattgta tgeecaaage ggtgetgta geetgtgt gagaectetgt tgaage 208 210 <210 > SEQ ID NO: 2 211  | 159 | 415     |        |       |            | 420   |       |       |       |            | 425   |        |        |       |            | 430   |              |
| 163  | 161 | gca tt  | g cca  | gct   | ctt        | сса   | atc   | tcc   | atc   | acc        | ttt   | ggg    | ctt    | gtt   | ttc        | tac   | 1586         |
| 165 ttt gcc aca gat tat ctt gta cag cct ttt atg gac caa tta gca ttc 166 Phe Ala Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe 167 450 455 460 169 cat caa ttt tat atc tagcatattt gcggttagaa tcccatggat gtttcttctt 1689 170 His Gln Phe Tyr Ile 171 465 173 tgactataac caaatctggg gaggacaaag gtgatttcc tgtgtccaca tctaacaaag 1749 175 tcaagattcc cggctggact tttgcagctt ccttccaagt cttcctgacc accttgcact 1809 177 attggacttt ggaaggaggt gcctatagaa aacgattttg aacatacttc atcgcagtgg 1869 179 actgtytccc tcggtgcaga aactaccaga tttgagggac gaggtcaagg agattagata 1929 181 ggcccggaag ttgctgtgcc ccatcagcag cttgaccgcg ggtcacagga cgattcact 1989 183 gacactgcga actctcagga ctaccaggta ccaagaggt aggtgaagg ggtttaaacca 2049 185 aacggaactc ttcatcttaa actacacgtt gaaaatcaac ccaataattc tgtattaaacc 2049 186 aacggaactc ttcatcttaa ggtactgtga ggaagagag gcaccagag cagaatggg gthe gagtgagagg gttcaaggag ggtacaagga gattacact 1989 189 aatggagagg tggcgaggg ttccagcttc cctttgattt tttgetgcag actcatcctt 2229 180 gcaattcttc ttctcaagca ctgacactca ttaccgtctg tgattgccat ttctcccaa 2349 181 ttaaatgay acttgtttc ccctcttt gagtcaagtc aaatatgtag attgcctttg 2289 189 gcaattctc ttctcaagca ctgacactca ttaccgtctg tgattgccat ttctcccaa 2349 189 ggcaagtctg aacctgaggt tyctttatcc tacaagttt aacctcaggt tccaaattc 2209 189 ggcaagtctg aacctgaggt tyctttatcc tacaagttt acctagtt gagtcaaat 2469 189 ttggatttc caccaaattc tgaatttgt gacatacttg tacgctcact tgcccccaag 2529 201 tgcctcctct gtcctcattc ttctcccac caccagcagt ctttttoac agccagaaa 2529 202 ttggatttc crtggtagca gatggtccca ttattctagg dtctactct ttgtatgatg 2649 203 gcagctctg crtggtagac gatggtccca ttattctagg dtctacctct ttgtatgatg 2649 205 aaaagaatgt gttatgaatc ggtgctgta gccctgctgt cagaactct tccacaagcaa 2709 207 atgagatgt tgcccaaagc ggtagaatta aagaagagta aaatggctgt tgaagc 2765 210 <210 > SEQ ID No: 2 211 <211 > LENGTH: 467 22 <212 > TYPE: PRT 213 <213 > ORGANISM: Homo sapiens 216 <400 > SEQUENCE: 2 217 Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met 218 1 5 10   | 162 | Ala Le  | ı Pro  | Ala   | Leu        | Pro   | Ile   | Ser   | Ile   | Thr        | Phe   | Gly    | Leu    | Val   | Phe        | Tyr   |              |
| 166  | 163 |         |        |       | 435        |       |       |       |       | 440        |       |        |        |       | 445        |       |              |
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| 197 gtaaattttg gaaacagtac agctatttct catcaattct ctatcatgtt gaagtcaaat 198 ttggatttc caccaaattc tgaatttgta gacatacttg tacgctcact tgccccaga 2529 201 tgcctcctct gtcctcattc ttctctccca cacaagcagt ctttttctac agccagtaag 2589 203 gcagctctgt crtggtagca gatggtccca ttattctagg gtcttactct ttgtatgatg 205 aaaagaatgt gttatgaatc ggtgctgtca gccctgctgt cagaccttct tccacagcaa 2709 207 atgagatgta tgcccaaagc ggtagaatta aagaagagta aaatggctgt tgaagc 2709 210 <210> SEQ ID NO: 2 211 <211> LENGTH: 467 212 <212> TYPE: PRT 213 <213> ORGANISM: Homo sapiens 216 <400> SEQUENCE: 2 217 Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met 218 1 5 10 15  | 193 | gcaatto | cttc   | ttct  | -<br>caago | ca ct | gaca  | actca | a tta | accgt      | ctg   | tgat   | itge   | cat   | ttctt      | cccaa | 2349         |
| 199 ttggatttte caceaaatte tgaatttgta gacatacttg tacgeteact tgeececaga 2529 201 tgeeteete gteeteatte tteteteea cacaageagt ettttetae ageeagtaag 2589 203 geagetetgt ertggtagea gatggteea ttattetagg gtettaetet ttgtatgatg 2649 205 aaaagaatgt gttatgaate ggtgetgtea geeetgetgt eagacettet teeacageaa 2709 207 atgagatgta tgeecaaage ggtagaatta aagaagagta aaatggetgt tgaage 2765 210 <210 > SEQ ID NO: 2 211 <211> LENGTH: 467 212 <212> TYPE: PRT 213 <213> ORGANISM: Homo sapiens 216 <400> SEQUENCE: 2 217 Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met 218 1 5 10 15  | 195 | ggccagt | ictg . | aacct | tgagg      | jt to | gcttt | catco | : taa | aaagt      | ttt   | aacc   | ctcag  | ggt 1 | tccaa      | attca | 2409         |
| 201 tgcctcctct gtcctcattc ttctctccca cacaagcagt ctttttctac agccagtaag 2589 203 gcagctctgt crtggtagca gatggtccca ttattctagg gtcttactct ttgtatgatg 2649 205 aaaagaatgt gttatgaatc ggtgctgtca gccctqctgt cagaccttct tccacagcaa 2709 207 atgagatgta tgcccaaagc ggtagaatta aagaagagta aaatggctgt tgaagc 2765 210 <210 > SEQ ID NO: 2 211 <211> LENGTH: 467 212 <212> TYPE: PRT 213 <213> ORGANISM: Homo sapiens 216 <400> SEQUENCE: 2 217 Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met 218 1 5 10 15   | 197 | gtaaati | ittg ( | gaaac | cagta      | ac ag | gctat | ttct  | t cat | caat       | tct   | ctat   | cate   | gtt   | gaagt      | caaat | 2469         |
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| 218 1 5 10 15  |     |         |        |       |            | Λlэ   | Dro   | Lou   | Sor   | Tur        | Dho   | Gln    | Δen    | Δla   | Gln        | Met   |              |
|  |     |         | . GIU  | LGU   |            | пта   | FIU   | Leu   | 261   |            | 1 116 | 0.111  | 63.011 | niu   |            | 1100  |              |
|  |     |         | ı Asp  | Asn   | -          | Leu   | Ser   | Asn   | Thr   |            | Arq   | Ser    | Gln    | Asn   |            | Asn   |              |

RAW SEQUENCE LISTING

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Output Set: N:\CRF4\11182002\1785474A.raw

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| 223        | Arg | Glu | Arg | Gln | Glu   | His | Asn | Asp | Arg | Arg | ser | Leu | Gly | His | Pro | Glu |
| 224        |     |     | 35  |     |       |     |     | 40  |     |     |     |     | 45  |     |     |     |
| 226        | Pro | Leu | Ser | Asn | Gly   | Arg | Pro | Gln | Gly | Asn | Ser | Arg | Gln | Val | Val | Glu |
| 227        |     | 50  |     |     | _     | _   | 55  |     |     |     |     | 60  |     |     |     |     |
| 229        | Gln | Asp | Glu | Glu | Glu   | Asp | Glu | Glu | Leu | Thr | Leu | Lys | Tyr | Gly | Ala | Lys |
| 230        |     | •   |     |     |       | 70  |     |     |     |     | 75  | •   | •   | -   |     | 80  |
| 232        | His | Val | Ile | Met | Leu   | Phe | Val | Pro | Val | Thr | Leu | Cys | Met | Val | Val | Val |
| 233        |     |     |     |     | 85    |     |     |     |     | 90  |     | •   |     |     | 95  |     |
|            | Val | Ala | Thr | Ile |       | Ser | Val | Ser | Phe | Tyr | Thr | Arq | Lys | Asp | Gly | Gln |
| 3 6 ئے     |     |     |     | 100 | 4     |     |     |     | 105 | 1   |     | ,   | 1   | 110 | _   |     |
|            | Leu | Ile | Tvr | Thr | Pro   | Phe | Thr | Glu | Asp | Thr | Glu | Thr | Val | Glv | Gln | Arq |
| <u></u> 39 |     |     | 115 |     |       |     |     | 120 |     |     |     |     | 125 | 1   |     |     |
|            | Ala | Leu |     | Ser | Ile   | Leu | Asn | Ala | Ala | Ile | Met | Ile | Ser | Val | Ile | Val |
| 242        |     | 130 |     |     |       |     | 135 |     |     |     |     | 140 |     |     |     |     |
|            | Val |     | Thr | Ile | Leu   | Leu | Val | Val | Leu | Tvr | Lys | Tvr | Arq | Cvs | Tyr | Lys |
|            | 145 |     |     |     |       | 150 |     |     |     | 1   | 155 | -   | ,   | •   | _   | 160 |
|            |     | He  | His | Ala | Trp   |     | Ile | Ile | Ser | Ser | Leu | Leu | Leu | Leu | Phe | Phe |
| 248        |     |     |     |     | 165   |     |     |     |     | 170 |     |     |     |     | 175 |     |
|            | Phe | Ser | Phe | Ile | Tvr   | Leu | Gly | Glu | Val | Phe | Lys | Thr | Tyr | Asn | Val | Ala |
| 251        |     |     |     | 180 | - 1 - |     | 1   |     | 185 |     |     |     | .4  | 190 |     |     |
|            | Val | Asp | Tvr |     | Thr   | Val | Ala | Leu |     | Ile | Trp | Asn | Phe | Gly | Val | Val |
| 254        |     | - 1 | 195 |     |       |     |     | 200 |     |     | •   |     | 205 | _   |     |     |
|            | Glv | Met | Ile | Ser | Ile   | His | Trp | Lvs | Glv | Pro | Leu | Arq | Leu | Gln | Gln | Ala |
| <b>257</b> | _   | 210 |     |     |       |     | 215 |     | -   |     |     | 220 |     |     |     |     |
|            | Tvr | Leu | Ile | Met | Ile   | Ser | Ala | Leu | Met | Ala | Leu | Val | Phe | Ile | Lys | Tyr |
| 260        | 225 |     |     |     |       | 230 |     |     |     |     | 235 |     |     |     | •   | 240 |
|            | Leu | Pro | Glu | Trp | Thr   | Ala | Trp | Leu | Ile | Leu |     | Val | Ile | Ser | Val | Tyr |
| 263        |     |     |     | -   | 245   |     |     |     |     | 250 |     |     |     |     | 255 | -   |
|            | Asp | Leu | Val | Ala | Val   | Leu | Cys | Pro | Lys | Gly | Pro | Leu | Arq | Met | Leu | Val |
| 266        | •   |     |     | 260 |       |     | •   |     | 265 | •   |     |     |     | 270 |     |     |
| 268        | Glu | Thr | Ala | Gln | Glu   | Arg | Asn | Glu | Thr | Leu | Phe | Pro | Ala | Leu | He  | Tyr |
| 269        |     |     | 275 |     |       |     |     | 280 |     |     |     |     | 285 |     |     |     |
| 271        | Ser | Ser | Thr | Met | Val   | Trp | Leu | Val | Asn | Met | Ala | Glu | Gly | Asp | Pro | Glu |
| 272        |     | 290 |     |     |       | _   | 295 |     |     |     |     | 300 | _   | _   |     |     |
| 274        | Ala | Gln | Arg | Arg | Val   | Ser | Lys | Asn | Ser | Lys | His | Asn | Ala | Glu | Ser | Thr |
|            | 305 |     |     | -   |       | 310 | -   |     |     | _   | 315 |     |     |     |     | 320 |
| 277        | Glu | Arg | Glu | Ser | Gln   | Asp | Thr | Val | Ala | Glu | Asn | Asp | Asp | Gly | Gly | Phe |
| 278        |     | _   |     |     | 325   |     |     |     |     | 330 |     |     |     |     | 335 |     |
| 280        | Ser | Glu | Glu | Trp | Glu   | Ala | Gln | Arg | Asp | Ser | His | Leu | Gly | Pro | His | Arg |
| 281        |     |     |     | 340 |       |     |     |     | 345 |     |     |     |     | 350 |     |     |
| 283        | Ser | Thr | Pro | Glu | Ser   | Arg | Ala | Ala | Val | Gln | Glu | Leu | Ser | Ser | Ser | Ile |
| 284        |     |     | 355 |     |       | -   |     | 360 |     |     |     |     | 365 |     |     |     |
| 286        | Leu | Ala | Gly | Glu | Asp   | Pro | Glu | Glu | Arg | Gly | Val | Lys | Leu | Gly | Leu | Gly |
| 287        |     | 370 | -   |     | -     |     | 375 |     | -   | -   |     | 380 |     | _   |     | •   |
| 289        | Asp | Phe | Ile | Phe | Tyr   | Ser | Val | Leu | Val | Gly | Lys | Ala | Ser | Ala | Thr | Ala |
| 290        | 385 |     |     |     |       | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| 292        | Ser | Gly | Asp | Trp | Asn   | Thr | Thr | He  | Ala | Cys | Phe | Val | Ala | Ile | Leu | Ile |
| 293        |     |     |     |     | 405   |     |     |     |     | 410 |     |     |     |     | 415 |     |

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Input Set : A:\Sub\_Seq\_List\_0609\_4180002.txt
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295 Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu 420 425 430 298 Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala 299 435 440 445 301 Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln 450 455 304 Phe Tyr Ile 305 465 308 <210> SEQ ID NO: 3 309 <211> LENGTH: 2765 310 <212> TYPE: DNA 311 <213> ORGANISM: Homo sapiens 314 <220> FEATURE: 315 <221> NAME/KEY: CDS 316 <222> LOCATION: (249)..(1649) 317 <223> OTHER INFORMATION: W--> 320 < 400> 3321 tyggacagge ageteegggg teegeggttt eacateggaa acaaaacage ggetggtetg 60 323 qaaqqaacct qaqctacqaq ccqcqqcqqc aqcqqqqqq cgqqqaaqcq tatacctaat 120 325 ctqqqaqcct qcaaqtqaca acaqcctttq cqqtccttag acaqcttggc ctggaggaga 180 327 acacatgaaa gaaagaacct caagaggett tgttttetgt gaaacagtat ttetatacag 240 329 tigotoca atg aca gag tia dot goa dog tig too tad tid dag aat goa 290 330 Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala 331 333 caq atg tot gag gac aac cac ctg agc aat act gta cgt agc cag aat 338 334 Gln Met Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn 335 15 2.0 386 337 gan aat aga gaa ogg dag gag dac aac gad aga ogg agd ott ggd dac 338 Asp Asn Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His 40 35 341 oct gag oca tta tot aat gga oga oco cag ggt aac too ogg dag gtg 434 342 Pro Glu Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val 343 50 55 482 345 gtg gag caa gat gag gaa gaa gat gag gag ctg aca ttg aaa tat ggc 346 Val Glu Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly 75 65 7.0 530 349 ged aag cat gtg ato atg etc ttt gtd eet gtg act etc tgd atg gtg 350 Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val 351 80 85 353 gtg gtc gtg gct acc att aag tca gtc agc ttt tat acc cgg aag gat 578 354 Val Val Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp 100 357 gag cag cta atc tat acc cca ttc aca gaa gat acc gag act gtg ggc 626 358 Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly 359 115 120 361 day aga goo otg dad toa att otg aat got god atd atg atd agt gto 674 362 Gln Arg Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val 3 fi 3 135 140 130

365 att git gic atg act atc cic cig gig git cig tat aaa tac agg tgc

722

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/785,474A

DATE: 11/18/2002 TIME: 12:52:36

Input Set : A:\Sub\_Seq\_List\_0609\_4180002.txt
Output Set: N:\CRF4\11182002\1785474A.raw

## Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the  $\langle 220 \rangle$  to  $\langle 223 \rangle$  fields of each sequence which presents at least one n or Xaa.

Seq#:25; Xaa Pos. 5